



#6

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Price, Laura A.
Pausch, Mark H.
- (ii) TITLE OF INVENTION: Potassium Channels, Nucleotide Sequences
Encoding Them, and Methods of Using Same
- (iii) NUMBER OF SEQUENCES: 56
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: American Home Products Corporation
 - (B) STREET: One Campus Drive
 - (C) CITY: Parsippany
 - (D) STATE: New Jersey
 - (E) COUNTRY: USA
 - (F) ZIP: 07054
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US
 - (B) FILING DATE: 11-MAR-1997
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Matthews, Gale F.
 - (B) REGISTRATION NUMBER: 32,269
 - (C) REFERENCE/DOCKET NUMBER: 32,421-C2
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 201-683-2134
 - (B) TELEFAX: 201-683-4117

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2441 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 190..2043

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ACGCGATCGC CGCGAGTGTA TATTTTTTTTT TTAGCTCAGT CTTCAGTGTT TCGCGATTCT	60
CTTTAAAAGA AAAAAAAAAAT AATAAGTCAA AACTACAAAC CACACAGCGA AAGGCGAAAG	120
CAACGGTTCC TGCGAGTGTT TATTTTTTTTT TTCAACAATT TTTGATCGTA GTGCGACAAT	180
CCGTCGAGC ATG TCG CCG AAT CGA TGG ATC CTG CTG CTC ATC TTC TAC	228

Met	Ser	Pro	Asn	Arg	Trp	Ile	Leu	Leu	Leu	Ile	Phe	Tyr				
1				5					10							
ATA	TCC	TAC	CTG	ATG	TTC	GGG	GCG	GCA	ATC	TAT	TAC	CAT	ATT	GAG	CAC	276
Ile	Ser	Tyr	Leu	Met	Phe	Gly	Ala	Ala	Ile	Tyr	Tyr	His	Ile	Glu	His	
15						20					25					
GGC	GAG	GAG	AAG	ATA	TCG	CGC	GCC	GAA	CAG	CGC	AAG	GCG	CAA	ATT	GCA	324
Gly	Glu	Glu	Lys	Ile	Ser	Arg	Ala	Glu	Gln	Arg	Lys	Ala	Gln	Ile	Ala	
30					35					40					45	
ATC	AAC	GAA	TAT	CTG	CTG	GAG	GAG	CTG	GGC	GAC	AAG	AAT	ACG	ACC	ACA	372
Ile	Asn	Glu	Tyr	Leu	Leu	Glu	Glu	Leu	Gly	Asp	Lys	Asn	Thr	Thr	Thr	
				50					55					60		
CAG	GAT	GAG	ATT	CTT	CAA	CGG	ATC	TCG	GAT	TAC	TGT	GAC	AAA	CCG	GTT	420
Gln	Asp	Glu	Ile	Leu	Gln	Arg	Ile	Ser	Asp	Tyr	Cys	Asp	Lys	Pro	Val	
			65					70					75			
ACA	TTG	CCG	CCG	ACA	TAT	GAT	GAT	ACG	CCC	TAC	ACG	TGG	ACC	TTC	TAC	468
Thr	Leu	Pro	Pro	Thr	Tyr	Asp	Asp	Thr	Pro	Tyr	Thr	Trp	Thr	Phe	Tyr	
		80					85					90				
CAT	GCC	TTC	TTC	TTC	GCC	TTC	ACC	GTT	TGC	TCC	ACG	GTG	GGA	TAT	GGG	516
His	Ala	Phe	Phe	Phe	Ala	Phe	Thr	Val	Cys	Ser	Thr	Val	Gly	Tyr	Gly	
95						100					105					
AAT	ATA	TCG	CCA	ACC	ACC	TTC	GCC	GGA	CGG	ATG	ATC	ATG	ATC	GCG	TAT	564
Asn	Ile	Ser	Pro	Thr	Thr	Phe	Ala	Gly	Arg	Met	Ile	Met	Ile	Ala	Tyr	
110					115					120				125		
TCG	GTG	ATT	GGC	ATC	CCC	GTC	AAT	GGT	ATC	CTC	TTT	GCC	GGC	CTC	GGC	612
Ser	Val	Ile	Gly	Ile	Pro	Val	Asn	Gly	Ile	Leu	Phe	Ala	Gly	Leu	Gly	
				130					135					140		
GAA	TAC	TTT	GGA	CGT	ACG	TTT	GAA	GCG	ATC	TAC	AGA	CGC	TAC	AAA	AAG	660
Glu	Tyr	Phe	Gly	Arg	Thr	Phe	Glu	Ala	Ile	Tyr	Arg	Arg	Tyr	Lys	Lys	
			145					150					155			
TAC	AAG	ATG	TCC	ACG	GAT	ATG	CAC	TAT	GTC	CCG	CCG	CAG	CTG	GGA	TTG	708
Tyr	Lys	Met	Ser	Thr	Asp	Met	His	Tyr	Val	Pro	Pro	Gln	Leu	Gly	Leu	
		160				165						170				
ATC	ACC	ACG	GTG	GTG	ATT	GCC	CTG	ATT	CCG	GGA	ATA	GCT	CTC	TTC	CTG	756
Ile	Thr	Thr	Val	Val	Ile	Ala	Leu	Ile	Pro	Gly	Ile	Ala	Leu	Phe	Leu	
	175					180					185					
GTG	CTG	CCC	TGC	GTG	GGT	GTT	CAC	CTA	CTT	CGA	GAA	CTG	GGC	CTA	TCT	804
Val	Leu	Pro	Cys	Val	Gly	Val	His	Leu	Leu	Arg	Glu	Leu	Gly	Leu	Ser	
190					195					200					205	
TCC	ATC	TCG	CTG	TAC	TAC	AGC	TAT	GTG	ACC	ACC	ACA	ACA	ATT	GGA	TTC	852
Ser	Ile	Ser	Leu	Tyr	Tyr	Ser	Tyr	Val	Thr	Thr	Thr	Thr	Ile	Gly	Phe	
				210					215					220		
GGT	GAC	TAT	GTG	CCC	ACA	TTT	GGA	GCC	AAC	CAG	CCC	AAG	GAG	TTC	GGC	900
Gly	Asp	Tyr	Val	Pro	Thr	Phe	Gly	Ala	Asn	Gln	Pro	Lys	Glu	Phe	Gly	
			225					230					235			
GGC	TGG	TTC	GTG	GTC	TAT	CAG	ATC	TTT	GTG	ATC	GTG	TGG	TTC	ATC	TTC	948
Gly	Trp	Phe	Val	Val	Tyr	Gln	Ile	Phe	Val	Ile	Val	Trp	Phe	Ile	Phe	
		240					245					250				
TCG	CTG	GGA	TAT	CTT	GTG	ATG	ATC	ATG	ACA	TTT	ATC	ACT	CGG	GGC	CTC	996
Ser	Leu	Gly	Tyr	Leu	Val	Met	Ile	Met	Thr	Phe	Ile	Thr	Arg	Gly	Leu	
	255					260					265					

CAG Gln 270	AGC Ser	AAG Lys	AAG Lys	CTG Leu	GCA Ala 275	TAC Tyr	CTG Leu	GAG Glu	CAG Gln 280	CAG Gln	TTG Leu	TCC Ser	TCC Ser	AAC Asn	CTG Leu 285	1044
AAG Lys	GCC Ala	ACA Thr	CAG Gln	AAT Asn 290	CGC Arg	ATC Ile	TGG Trp	TCT Ser	GGC Gly 295	GTC Val	ACC Thr	AAG Lys	GAT Asp	GTG Val 300	GGC Gly	1092
TAC Tyr	CTC Leu	CGG Arg	CGA Arg 305	ATG Met	CTC Leu	AAC Asn	GAG Glu 310	CTG Leu 310	TAC Tyr	ATC Ile	CTC Leu	AAA Lys 315	GTG Val 315	AAG Lys	CCT Pro	1140
GTG Val	TAC Tyr	ACC Thr 320	GAT Asp	GTA Val	GAT Asp	ATC Ile	GCC Ala 325	TAC Tyr	ACA Thr	CTG Leu	CCA Pro	CGT Arg 330	TCC Ser	AAT Asn	TCG Ser	1188
TGT Cys 335	CCG Pro	GAT Asp	CTG Leu	AGC Ser	ATG Met	TAC Tyr 340	CGC Arg	GTG Val	GAG Glu	CCG Pro	GCT Ala 345	CCC Pro	ATT Ile	CCC Pro	AGC Ser	1236
CGG Arg 350	AAG Lys	AGG Arg	GCA Ala	TTC Phe	TCC Ser 355	GTG Val	TGC Cys	GCC Ala	GAC Asp 360	ATG Met	GTT Val	GGC Gly	GCC Ala	CAA Gln	AGG Arg 365	1284
GAG Glu	GCG Ala	GGC Gly	ATG Met 370	GTA Val	CAC His	GCC Ala	AAT Asn	TCC Ser	GAT Asp 375	ACG Thr	GAT Asp	CTA Leu	ACC Thr	AAA Lys 380	CTG Leu	1332
GAT Asp	CGC Arg	GAG Glu	AAG Lys 385	ACA Thr	TTC Phe	GAG Glu	ACG Thr	GCG Ala 390	GAG Glu	GCG Ala	TAC Tyr	CAC His	CAG Gln 395	ACC Thr	ACC Thr	1380
GAT Asp	TTG Leu 400	CTG Leu	GCC Ala	AAG Lys	GTG Val	GTC Val	AAC Asn 405	GCA Ala	CTG Leu	GCC Ala	ACG Thr	GTG Val 410	AAG Lys	CCA Pro	CCG Pro	1428
CCG Pro 415	GCG Ala	GAA Glu	CAG Gln	GAA Glu	GAT Asp	GCG Ala 420	GCT Ala	CTC Leu	TAT Tyr	GGT Gly	GGC Gly 425	TAT Tyr	CAT His	GGC Gly	TTC Phe	1476
TCC Ser 430	GAC Asp	TCC Ser	CAG Gln	ATC Ile	CTG Leu 435	GCC Ala	AGC Ser	GAA Glu	TGG Trp	TCG Ser 440	TTC Phe	TCG Ser	ACG Thr	GTC Val	AAC Asn 445	1524
GAG Glu	TTC Phe	ACA Thr	TCA Ser	CCG Pro 450	CGA Arg	CGT Arg	CCA Pro	AGA Arg	GCA Ala 455	CGT Arg	GCC Ala	TGC Cys	TCC Ser	GAT Asp 460	TTC Phe	1572
AAT Asn	CTG Leu	GAG Glu	GCA Ala 465	CCT Pro	CGC Arg	TGG Trp	CAG Gln 470	AGC Ser	GAG Glu	AGG Arg	CCA Pro	CTG Leu	CGT Arg 475	TCG Ser	AGC Ser	1620
CAC His	AAC Asn 480	GAA Glu	TGG Trp	ACA Thr	TGG Trp	AGC Ser	GGC Gly 485	GAC Asp	AAC Asn	CAG Gln	CAG Gln	ATC Ile 490	CAG Gln	GAG Glu	GCA Ala	1668
TTC Phe 495	AAC Asn	CAG Gln	CGC Arg	TAC Tyr	AAG Lys	GGA Gly 500	CAG Gln	CAG Gln	CGT Arg	GCC Ala	AAC Asn 505	GGA Gly	GCA Ala	GCC Ala	AAC Asn	1716
TCG Ser 510	ACC Thr	ATG Met	GTC Val	CAT His	CTG Leu 515	GAG Glu	CCG Pro	GAT Asp	GCT Ala	TTG Leu 520	GAG Glu	GAG Glu	CAG Gln	CTG Leu 525	AGA Arg	1764
AAC	AAT	CAC	CGG	GTG	CCG	GTC	GCG	TCA	AGA	AGT	TCT	CCA	TGC	CGG	ATG	1812

Asn	Asn	His	Arg	Val	Pro	Val	Ala	Ser	Arg	Ser	Ser	Pro	Cys	Arg	Met	
				530					535					540		
GTC	TGC	GAC	GTC	TGT	TTC	CCT	TCC	AGA	AGA	AGC	ACC	CCT	CGC	AGG	ATC	1860
Val	Cys	Asp	Val	Cys	Phe	Pro	Ser	Arg	Arg	Ser	Thr	Pro	Arg	Arg	Ile	
			545					550					555			
TGG	AGC	GCA	AGT	TGT	CCG	TGG	TCT	CGG	TAC	CCG	AGG	GTG	TCA	TCT	CGC	1908
Trp	Ser	Ala	Ser	Cys	Pro	Trp	Ser	Arg	Tyr	Pro	Arg	Val	Ser	Ser	Arg	
		560					565					570				
AGG	AAG	CCA	GAT	CCC	CGC	TGG	ACT	ACT	ACA	TCA	ACA	CGG	TCA	CGG	CGG	1956
Arg	Lys	Pro	Asp	Pro	Arg	Trp	Thr	Thr	Thr	Ser	Thr	Arg	Ser	Arg	Arg	
	575					580				585						
CCT	CCA	GTC	AAT	CCT	ATT	TGC	GCA	ACG	GAC	GCG	GTC	CGC	CAC	CGC	CCT	2004
Pro	Pro	Val	Asn	Pro	Ile	Cys	Ala	Thr	Asp	Ala	Val	Arg	His	Arg	Pro	
590					595					600					605	
TCG	AAT	CGA	ATG	GCA	GCT	TGG	CCA	GCG	GCG	GCG	GCG	GGC	TAACGAACAT			2053
Ser	Asn	Arg	Met	Ala	Ala	Trp	Pro	Ala	Ala	Ala	Ala	Gly				
				610					615							
GGGCTTCCAG	ATGGAGGATG	GAGCAACCCC	GCCATCGGCA	TTGGGCGGTG	GAGCCTATCA											2113
ACGCAAGGCG	GCTGCTGGCA	AGCGCCGACG	CGAGAGCATC	TACACCCAGA	ATCAAGCCCC											2173
ATCCGCTCGC	CGGGGCAGCA	TGTATCCGCC	GACCGCGCAC	GCCTTGGCCC	AGATGCAGAT											2233
GCGACGCGGC	AGCTTGGCAA	CCAGTGGCTC	TGGATCGGCG	GCCATGGCGG	CAGTGGCCGC											2293
GCGTCGTGGC	AGCCTCTTCC	CAGCTACAGC	ATCGGCATCA	TCGCTGACCT	CTGCTCCGCG											2353
CCGAAGCAGC	ATATTCTCGG	TTACCTCCGA	AAAGGATATG	AATGTGCTGG	AGCAGACGAC											2413
CATTGCGGAT	CTGATTCGTG	CGCTCGAG														2441

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 618 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Ser	Pro	Asn	Arg	Trp	Ile	Leu	Leu	Leu	Ile	Phe	Tyr	Ile	Ser	Tyr
1				5					10					15	
Leu	Met	Phe	Gly	Ala	Ala	Ile	Tyr	Tyr	His	Ile	Glu	His	Gly	Glu	Glu
		20					25						30		
Lys	Ile	Ser	Arg	Ala	Glu	Gln	Arg	Lys	Ala	Gln	Ile	Ala	Ile	Asn	Glu
	35						40					45			
Tyr	Leu	Leu	Glu	Glu	Leu	Gly	Asp	Lys	Asn	Thr	Thr	Thr	Gln	Asp	Glu
	50					55					60				
Ile	Leu	Gln	Arg	Ile	Ser	Asp	Tyr	Cys	Asp	Lys	Pro	Val	Thr	Leu	Pro
65					70					75				80	
Pro	Thr	Tyr	Asp	Asp	Thr	Pro	Tyr	Thr	Trp	Thr	Phe	Tyr	His	Ala	Phe
			85						90					95	

Phe	Phe	Ala	Phe	Thr	Val	Cys	Ser	Thr	Val	Gly	Tyr	Gly	Asn	Ile	Ser		
			100					105					110				
Pro	Thr	Thr	Phe	Ala	Gly	Arg	Met	Ile	Met	Ile	Ala	Tyr	Ser	Val	Ile		
		115					120					125					
Gly	Ile	Pro	Val	Asn	Gly	Ile	Leu	Phe	Ala	Gly	Leu	Gly	Glu	Tyr	Phe		
	130					135					140						
Gly	Arg	Thr	Phe	Glu	Ala	Ile	Tyr	Arg	Arg	Tyr	Lys	Lys	Tyr	Lys	Met		
145				150						155					160		
Ser	Thr	Asp	Met	His	Tyr	Val	Pro	Pro	Gln	Leu	Gly	Leu	Ile	Thr	Thr		
				165					170					175			
Val	Val	Ile	Ala	Leu	Ile	Pro	Gly	Ile	Ala	Leu	Phe	Leu	Val	Leu	Pro		
			180					185					190				
Cys	Val	Gly	Val	His	Leu	Leu	Arg	Glu	Leu	Gly	Leu	Ser	Ser	Ile	Ser		
		195					200					205					
Leu	Tyr	Tyr	Ser	Tyr	Val	Thr	Thr	Thr	Thr	Ile	Gly	Phe	Gly	Asp	Tyr		
	210					215					220						
Val	Pro	Thr	Phe	Gly	Ala	Asn	Gln	Pro	Lys	Glu	Phe	Gly	Gly	Trp	Phe		
225					230					235					240		
Val	Val	Tyr	Gln	Ile	Phe	Val	Ile	Val	Trp	Phe	Ile	Phe	Ser	Leu	Gly		
				245					250					255			
Tyr	Leu	Val	Met	Ile	Met	Thr	Phe	Ile	Thr	Arg	Gly	Leu	Gln	Ser	Lys		
			260					265					270				
Lys	Leu	Ala	Tyr	Leu	Glu	Gln	Gln	Leu	Ser	Ser	Asn	Leu	Lys	Ala	Thr		
		275					280					285					
Gln	Asn	Arg	Ile	Trp	Ser	Gly	Val	Thr	Lys	Asp	Val	Gly	Tyr	Leu	Arg		
	290					295					300						
Arg	Met	Leu	Asn	Glu	Leu	Tyr	Ile	Leu	Lys	Val	Lys	Pro	Val	Tyr	Thr		
305					310					315					320		
Asp	Val	Asp	Ile	Ala	Tyr	Thr	Leu	Pro	Arg	Ser	Asn	Ser	Cys	Pro	Asp		
				325					330					335			
Leu	Ser	Met	Tyr	Arg	Val	Glu	Pro	Ala	Pro	Ile	Pro	Ser	Arg	Lys	Arg		
			340					345					350				
Ala	Phe	Ser	Val	Cys	Ala	Asp	Met	Val	Gly	Ala	Gln	Arg	Glu	Ala	Gly		
		355					360					365					
Met	Val	His	Ala	Asn	Ser	Asp	Thr	Asp	Leu	Thr	Lys	Leu	Asp	Arg	Glu		
	370					375					380						
Lys	Thr	Phe	Glu	Thr	Ala	Glu	Ala	Tyr	His	Gln	Thr	Thr	Asp	Leu	Leu		
385					390					395				400			
Ala	Lys	Val	Val	Asn	Ala	Leu	Ala	Thr	Val	Lys	Pro	Pro	Pro	Ala	Glu		
				405					410					415			
Gln	Glu	Asp	Ala	Ala	Leu	Tyr	Gly	Gly	Tyr	His	Gly	Phe	Ser	Asp	Ser		
			420					425					430				
Gln	Ile	Leu	Ala	Ser	Glu	Trp	Ser	Phe	Ser	Thr	Val	Asn	Glu	Phe	Thr		
		435					440					445					

Ser Pro Arg Arg Pro Arg Ala Arg Ala Cys Ser Asp Phe Asn Leu Glu
 450 455 460
 Ala Pro Arg Trp Gln Ser Glu Arg Pro Leu Arg Ser Ser His Asn Glu
 465 470 475 480
 Trp Thr Trp Ser Gly Asp Asn Gln Gln Ile Gln Glu Ala Phe Asn Gln
 485 490 495
 Arg Tyr Lys Gly Gln Gln Arg Ala Asn Gly Ala Ala Asn Ser Thr Met
 500 505 510
 Val His Leu Glu Pro Asp Ala Leu Glu Glu Gln Leu Arg Asn Asn His
 515 520 525
 Arg Val Pro Val Ala Ser Arg Ser Ser Pro Cys Arg Met Val Cys Asp
 530 535 540
 Val Cys Phe Pro Ser Arg Arg Ser Thr Pro Arg Arg Ile Trp Ser Ala
 545 550 555 560
 Ser Cys Pro Trp Ser Arg Tyr Pro Arg Val Ser Ser Arg Arg Lys Pro
 565 570 575
 Asp Pro Arg Trp Thr Thr Thr Ser Thr Arg Ser Arg Arg Pro Pro Val
 580 585 590
 Asn Pro Ile Cys Ala Thr Asp Ala Val Arg His Arg Pro Ser Asn Arg
 595 600 605
 Met Ala Ala Trp Pro Ala Ala Ala Ala Gly
 610 615

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1011 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1008

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATG	TCC	GAT	CAG	CTG	TTT	GTC	GCA	TTT	GAG	AAG	TAT	TTC	TTG	ACG	AGT	48
Met	Ser	Asp	Gln	Leu	Phe	Val	Ala	Phe	Glu	Lys	Tyr	Phe	Leu	Thr	Ser	
1				5					10					15		
AAC	GAG	GTC	AAG	AAG	AAT	GCA	GCA	ACG	GAG	ACA	TGG	ACA	TTT	TCA	TCG	96
Asn	Glu	Val	Lys	Lys	Asn	Ala	Ala	Thr	Glu	Thr	Trp	Thr	Phe	Ser	Ser	
			20					25					30			
TCC	ATT	TTC	TTT	GCC	GTA	ACC	GTC	GTC	ACT	ACC	ATC	GGA	TAC	GGT	AAT	144
Ser	Ile	Phe	Phe	Ala	Val	Thr	Val	Val	Thr	Thr	Ile	Gly	Tyr	Gly	Asn	
			35				40					45				
CCA	GTT	CCA	GTG	ACA	AAC	ATT	GGA	CGG	ATA	TGG	TGT	ATA	TTG	TTC	TCC	192
Pro	Val	Pro	Val	Thr	Asn	Ile	Gly	Arg	Ile	Trp	Cys	Ile	Leu	Phe	Ser	
			50			55					60					

TTG CTT GGA ATA CCT CTA ACA CTG GTT ACC ATC GCT GAC TTG GCA GGT	240
Leu Leu Gly Ile Pro Leu Thr Leu Val Thr Ile Ala Asp Leu Ala Gly	
65 70 75 80	
AAA TTC CTA TCT GAA CAT CTT GTT TGG TTG TAT GGA AAC TAT TTG AAA	288
Lys Phe Leu Ser Glu His Leu Val Trp Leu Tyr Gly Asn Tyr Leu Lys	
85 90 95	
TTA AAA TAT CTC ATA TTG TCA CGA CAT CGA AAA GAA CGG AGA GAG CAC	336
Leu Lys Tyr Leu Ile Leu Ser Arg His Arg Lys Glu Arg Arg Glu His	
100 105 110	
GTT TGT GAG CAC TGT CAC AGT CAT GGA ATG GGG CAT GAT ATG AAT ATC	384
Val Cys Glu His Cys His Ser His Gly Met Gly His Asp Met Asn Ile	
115 120 125	
GAG GAG AAA AGA ATT CCT GCA TTC CTG GTA TTA GCT ATT CTG ATA GTA	432
Glu Glu Lys Arg Ile Pro Ala Phe Leu Val Leu Ala Ile Leu Ile Val	
130 135 140	
TAT ACA GCG TTT GGC GGT GTC CTA ATG TCA AAA TTA GAG CCG TGG TCT	480
Tyr Thr Ala Phe Gly Gly Val Leu Met Ser Lys Leu Glu Pro Trp Ser	
145 150 155 160	
TTC TTC ACT TCA TTC TAC TGG TCC TTC ATT ACA ATG ACT ACT GTC GGG	528
Phe Phe Thr Ser Phe Tyr Trp Ser Phe Ile Thr Met Thr Thr Val Gly	
165 170 175	
TTT GGC GAC TTG ATG CCC AGA AGG GAC GGA TAC ATG TAT ATC ATA TTG	576
Phe Gly Asp Leu Met Pro Arg Arg Asp Gly Tyr Met Tyr Ile Ile Leu	
180 185 190	
CTC TAT ATC ATT TTA GGT AAA TTT TCA ATG AAA AAA AAA CAA AAA TTC	624
Leu Tyr Ile Ile Leu Gly Lys Phe Ser Met Lys Lys Lys Gln Lys Phe	
195 200 205	
AAA ATA TTT TTA GGT CTT GCA ATA ACT ACA ATG TGC ATT GAT TTG GTA	672
Lys Ile Phe Leu Gly Leu Ala Ile Thr Thr Met Cys Ile Asp Leu Val	
210 215 220	
GGA GTA CAG TAT ATT CGA AAG ATT CAT TAT TTC GGA AGA AAA ATT CAA	720
Gly Val Gln Tyr Ile Arg Lys Ile His Tyr Phe Gly Arg Lys Ile Gln	
225 230 235 240	
GAC GCT AGA TCT GCA TTG GCG GTT GTA GGA GGA AAG GTA GTC CTT GTA	768
Asp Ala Arg Ser Ala Leu Ala Val Val Gly Gly Lys Val Val Leu Val	
245 250 255	
TCA GAA CTC TAC GCA AAT TTA ATG CAA AAG CGA GCT CGT AAC ATG TCC	816
Ser Glu Leu Tyr Ala Asn Leu Met Gln Lys Arg Ala Arg Asn Met Ser	
260 265 270	
CGA GAA GCT TTT ATA GTG GAG AAT CTC TAT GTT TCC AAA CAC ATC ATA	864
Arg Glu Ala Phe Ile Val Glu Asn Leu Tyr Val Ser Lys His Ile Ile	
275 280 285	
CCA TTC ATA CCA ACT GAT ATC CGA TGT ATT CGA TAT ATT GAT CAA ACT	912
Pro Phe Ile Pro Thr Asp Ile Arg Cys Ile Arg Tyr Ile Asp Gln Thr	
290 295 300	
GCC GAT GCT GCT ACC ATT TCC ACG TCA TCG TCT GCA ATT GAT ATG CAA	960
Ala Asp Ala Ala Thr Ile Ser Thr Ser Ser Ser Ala Ile Asp Met Gln	
305 310 315 320	
AGT TGT AGA TTT TGT CAT TCA AGA TAT TCT CTC AAT CGT GCA TTC AAA	1008

Ser Cys Arg Phe Cys His Ser Arg Tyr Ser Leu Asn Arg Ala Phe Lys
 325 330 335

TAG

1011

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Ser	Asp	Gln	Leu	Phe	Val	Ala	Phe	Glu	Lys	Tyr	Phe	Leu	Thr	Ser	1	5	10	15
Asn	Glu	Val	Lys	Lys	Asn	Ala	Ala	Thr	Glu	Thr	Trp	Thr	Phe	Ser	Ser	20	25	30	
Ser	Ile	Phe	Phe	Ala	Val	Thr	Val	Val	Thr	Thr	Ile	Gly	Tyr	Gly	Asn	35	40	45	
Pro	Val	Pro	Val	Thr	Asn	Ile	Gly	Arg	Ile	Trp	Cys	Ile	Leu	Phe	Ser	50	55	60	
Leu	Leu	Gly	Ile	Pro	Leu	Thr	Leu	Val	Thr	Ile	Ala	Asp	Leu	Ala	Gly	65	70	75	80
Lys	Phe	Leu	Ser	Glu	His	Leu	Val	Trp	Leu	Tyr	Gly	Asn	Tyr	Leu	Lys	85	90	95	
Leu	Lys	Tyr	Leu	Ile	Leu	Ser	Arg	His	Arg	Lys	Glu	Arg	Arg	Glu	His	100	105	110	
Val	Cys	Glu	His	Cys	His	Ser	His	Gly	Met	Gly	His	Asp	Met	Asn	Ile	115	120	125	
Glu	Glu	Lys	Arg	Ile	Pro	Ala	Phe	Leu	Val	Leu	Ala	Ile	Leu	Ile	Val	130	135	140	
Tyr	Thr	Ala	Phe	Gly	Gly	Val	Leu	Met	Ser	Lys	Leu	Glu	Pro	Trp	Ser	145	150	155	160
Phe	Phe	Thr	Ser	Phe	Tyr	Trp	Ser	Phe	Ile	Thr	Met	Thr	Thr	Val	Gly	165	170	175	
Phe	Gly	Asp	Leu	Met	Pro	Arg	Arg	Asp	Gly	Tyr	Met	Tyr	Ile	Ile	Leu	180	185	190	
Leu	Tyr	Ile	Ile	Leu	Gly	Lys	Phe	Ser	Met	Lys	Lys	Lys	Gln	Lys	Phe	195	200	205	
Lys	Ile	Phe	Leu	Gly	Leu	Ala	Ile	Thr	Thr	Met	Cys	Ile	Asp	Leu	Val	210	215	220	
Gly	Val	Gln	Tyr	Ile	Arg	Lys	Ile	His	Tyr	Phe	Gly	Arg	Lys	Ile	Gln	225	230	235	240
Asp	Ala	Arg	Ser	Ala	Leu	Ala	Val	Val	Gly	Gly	Lys	Val	Val	Leu	Val	245	250	255	
Ser	Glu	Leu	Tyr	Ala	Asn	Leu	Met	Gln	Lys	Arg	Ala	Arg	Asn	Met	Ser				

260	265	270
Arg Glu Ala Phe Ile Val Glu Asn Leu Tyr Val Ser Lys His Ile Ile		
275	280	285
Pro Phe Ile Pro Thr Asp Ile Arg Cys Ile Arg Tyr Ile Asp Gln Thr		
290	295	300
Ala Asp Ala Ala Thr Ile Ser Thr Ser Ser Ser Ala Ile Asp Met Gln		
305	310	315
Ser Cys Arg Phe Cys His Ser Arg Tyr Ser Leu Asn Arg Ala Phe Lys		
325	330	335

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 51 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TCCATTTTCT TTGCCGTAAC CGTCGTCACT ACCATCGGAT ACGGTAATCC A 51

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 51 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TCATTCTACT GGTCTTCAT TACAATGACT ACTGTCGGGT TTGGCGACTT G 51

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Ala Phe Leu Phe Ser Ile Glu Thr Gln Thr Thr Ile Gly Tyr Gly Phe
1 5 10 15
Arg Cys Val Thr Asp Glu Cys Pro
20

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ala Phe Leu Phe Ser Leu Glu Thr Gln Val Thr Ile Gly Tyr Gly Phe
1 5 10 15
Arg Cys Val Thr Glu Gln Cys Ala
 20

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Ala Phe Leu Phe Phe Ile Glu Thr Glu Ala Thr Ile Gly Tyr Gly Tyr
1 5 10 15
Arg Tyr Ile Thr Asp His Cys Pro
 20

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Ala Phe Phe Phe Ala Phe Thr Val Cys Ser Thr Val Gly Tyr Gly Asn
1 5 10 15
Ile Ser Pro Thr Thr Phe Ala Gly
 20

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Ala Phe Trp Trp Ala Val Val Thr Met Thr Thr Val Gly Tyr Gly Asp
1 5 10 15

Met Thr Pro Val Gly Phe Trp Gly
20

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Ala Phe Trp Tyr Thr Ile Val Thr Met Thr Thr Leu Gly Tyr Gly Asp
1 5 10 15

Met Val Pro Glu Thr Ile Ala Gly
20

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Ala Phe Trp Trp Ala Gly Ile Thr Met Thr Thr Val Gly Tyr Gly Asp
1 5 10 15

Ile Cys Pro Thr Thr Ala Leu Gly
20

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Gly Leu Trp Trp Ala Leu Val Thr Met Thr Thr Val Gly Tyr Gly Asp
1 5 10 15

Met Ala Pro Lys Thr Tyr Ile Gly
20

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Ala Leu Tyr Phe Thr Met Thr Cys Met Thr Ser Val Gly Phe Gly Asn
1 5 10 15

Val Ala Ala Glu Thr Asp Asn Glu
 20

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Cys Val Tyr Phe Leu Ile Val Thr Met Ser Thr Val Gly Tyr Gly Asp
1 5 10 15

Val Tyr Cys Glu Thr Val Leu Gly
 20

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Ser Leu Tyr Thr Ser Tyr Val Thr Thr Thr Thr Ile Gly Phe Gly Asp
1 5 10 15

Tyr Val Pro Thr Phe Gly Ala Asn
 20

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Ala Phe Phe Phe Ala Phe Thr Val Cys Ser Thr Val Gly Tyr Gly Asn
1 5 10 15

Ile Ser Pro Thr Thr Phe Ala Gly
20

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Ser Ile Phe Phe Ala Val Thr Val Val Thr Thr Ile Gly Tyr Gly Asn
1 5 10 15

Pro Val Pro Val Thr Asn Thr Gly
20

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Ser Leu Tyr Thr Ser Tyr Val Thr Thr Thr Thr Ile Gly Phe Gly Asp
1 5 10 15

Tyr Val Pro Thr Phe Gly Ala Asn
20

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Ser Phe Tyr Trp Ser Phe Ile Thr Met Thr Thr Val Gly Phe Gly Asp
1 5 10 15

Leu Met Pro Arg Arg Asp Gly Tyr
20

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ATAAAGCTTA AAAATGTCGC CGAATCGATG GAT

33

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

AGCTCTAGAC CTCCATCTGG AAGCCCATGT

30

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

AAAAAGCTTA AAATGGCACA CATCACG

27

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

AAACTCGAGT CATACTGTG GACT

24

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

AAAAAGCTTA AAATGGTCGG GCAATTG

27

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

AAAAGCATGC TCATCTGGAT GGGCA

25

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AAAAAGCTTA AAATGGCCTC GGTCGCC

27

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

TTTTCTAGAC TACATCGTTG TCTT

24

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

AAAAAGCTTA AAATGAATCT GATCAAC

27

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

AAATCTAGAT TAGTCGAAAC TGAA

24

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

AAAAAGCTTA AAATGCCTGG CGGA

24

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

AAATCTAGAG GCTACAGGAA GTCC

24

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GGGGGTACCA AAATGTCGGG GTGTGAT

27

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

TTTTTCTAGA TCAAGAGTTA TCATC

25

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1394 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

ATGGTAATAA TCAACCGATC GAACACCTAT GCCGTTGAGC AGGAAGCATT TCCAAGAGAC	60
AAGTACAATA TTGTCTACTG GCTCGTCATT CTTGTTGGAT TCGGAGTTCT TCTGCCATGG	120
AATATGTTCA TTACTATCGC CCCTGAGTAT TATGTGAATT ATTGGTTCAA ACCGGATGGC	180
GTGGAGACAT GGTATTCGAA AGAATTCATG GGATCTTTGA CGATTGGCTC ACAACTTCCA	240
AACGCAAGCA TTAATGTTTT CAACCTGTTC CTCATTATTG CTGGTCCCCT GATCTACCGC	300
GTCTTTGCTC CGGTTTGCTT CAACATCGTC AACCTGACAA TCATTCTCAT CCTCGTCATT	360
GTTCTGGAGC CCACTGAAGA TTCCATGTCC TGGTTTTTCT GGGTAACTCT TGGAATGGCG	420
ACTTCAATCA ATTTTAGCAA TGGGCTATAT GAAAACTCGG TTTATGGAGT TGGTGGCGAT	480
TTTCCGCACA CCTACATTGG CGCTCTCTTG ATTGGAAACA ACATTTGCGG ATTGCTGATA	540
ACGGTTGTGA AAATCGGAGT GACCTATTTT CTGAATGATG AGCCTAAACT TGTTGCAATC	600
GTCTATTTTCG GCATATCGTT GGTGATCCTT CTGGTGTGTG CAATTGCACT TTTCTTTATC	660
ACAAAGCAAG ATTTCTACCA CTATCACCAT CAAAAAGGAA TGGAAATTCG CGAAAAGGCG	720
GAAACCGACA GACCGTCTCC ATCCATTCTT TGGACCACAT TCACAACTG TTATGGGCAA	780
CTCTTCAATG TTTGGTTCTG CTTTGCCGTT ACTCTCACA TCTTCCCTGT TATGATGACC	840
GTTACCACTC GTGGAGATTC CGGCTTCCTA AACAAAATTA TGTCTGAAAA CGATGAAATC	900
TACACTTTGC TCACAAGTTT CCTCGTCTTC AATTTGTTTC CTGCGATTGG ATCCATAGTT	960
GCTTCCAAGA TTTACTGGCC GACACCCCGT TACCTCAAAT TTGCCATAAT CTTGCGTGCT	1020
CTTTTCATTC CATTCTTCTT CTTCTGCAAC TATCGTGTCC AGACGCGTGC TTATCCTGTT	1080
TTCTTTGAGT CTA CTGACAT TTTTGTGATT GGTGGAATTG CCATGTCTTT TTCACATGGA	1140
TACCTCAGCG CTCTGGCAAT GGGATACACT CCAAACGTCG TGCCATCTCA CTACTCAAGA	1200

TTTGCCGCTC AGCTTTCCGT TTGACTCTT ATGGTTGGCC TTCTCACCGG TGGCCTGTGG 1260
 CCCGTTGTTA TTGAGCACTT CGTGGACAAG CCAAGTATCT TATAAATATT TATAGCATTA 1320
 GAGTATACTT GTTATATGTT GTTTTTATTA AGCTGTGGAA TAAAATAATT ATTAAAAAAA 1380
 AAAAAAAAAA AAAA 1394

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Met	Ser	Pro	Asn	Arg	Trp	Ile	Leu	Leu	Leu	Ile	Phe	Tyr	Ile	Ser	Tyr	1	5	10	15
Leu	Met	Phe	Gly	Ala	Ala	Ile	Tyr	Tyr	His	Ile	Glu	His	Gly	Glu	Glu	20	25	30	
Lys	Ile	Ser	Arg	Ala	Glu	Gln	Arg	Lys	Ala	Gln	Ile	Ala	Ile	Asn	Glu	35	40	45	
Tyr	Leu	Leu	Glu	Glu	Leu	Gly	Asp	Lys	Asn	Thr	Thr	Thr	Gln	Asp	Glu	50	55	60	
Ile	Leu	Gln	Arg	Ile	Ser	Asp	Tyr	Cys	Asp	Lys	Pro	Val	Thr	Leu	Pro	65	70	75	80
Pro	Thr	Tyr	Asp	Asp	Thr	Pro	Tyr	Thr	Trp	Thr	Phe	Tyr	His	Ala	Phe	85	90	95	
Phe	Phe	Ala	Phe	Thr	Val	Cys	Ser	Thr	Val	Gly	Tyr	Gly	Asn	Ile	Ser	100	105	110	
Pro	Thr	Thr	Phe	Ala	Gly	Arg	Met	Ile	Met	Ile	Ala	Tyr	Ser	Val	Ile	115	120	125	
Gly	Ile	Pro	Val	Asn	Gly	Ile	Leu	Phe	Ala	Gly	Leu	Gly	Glu	Tyr	Phe	130	135	140	
Gly	Arg	Thr	Phe	Glu	Ala	Ile	Tyr	Arg	Arg	Tyr	Lys	Lys	Tyr	Lys	Met	145	150	155	160
Ser	Thr	Asp	Met	His	Tyr	Val	Pro	Pro	Gln	Leu	Gly	Leu	Ile	Thr	Thr	165	170	175	
Val	Val	Ile	Ala	Leu	Ile	Pro	Gly	Ile	Ala	Leu	Phe	Leu	Val	Leu	Pro	180	185	190	
Cys	Val	Gly	Val	His	Leu	Leu	Arg	Glu	Leu	Gly	Leu	Ser	Ser	Ile	Ser	195	200	205	
Leu	Tyr	Tyr	Ser	Tyr	Val	Thr	Ile	Thr	Thr	Ile	Gly	Phe	Gly	Asp	Tyr	210	215	220	
Val	Pro	Thr	Phe	Gly	Ala	Asn	Gln	Pro	Lys	Glu	Phe	Gly	Gly	Trp	Phe	225	230	235	240

Val	Val	Tyr	Gln	Ile	Phe	Val	Ile	Val	Trp	Phe	Ile	Phe	Ser	Leu	Gly	
				245					250					255		
Tyr	Leu	Val	Met	Ile	Met	Thr	Phe	Ile	Thr	Arg	Gly	Leu	Gln	Ser	Lys	
			260					265					270			
Lys	Leu	Ala	Tyr	Leu	Glu	Gln	Gln	Leu	Ser	Ser	Asn	Leu	Lys	Ala	Thr	
		275					280					285				
Gln	Asn	Arg	Ile	Trp	Ser	Gly	Val	Thr	Lys	Asp	Val	Gly	Tyr	Leu	Arg	
	290					295					300					
Arg	Met	Leu	Asn	Glu	Leu	Tyr	Ile	Leu	Lys	Val	Lys	Pro	Val	Tyr	Thr	
305				310						315					320	
Asp	Val	Asp	Ile	Ala	Tyr	Thr	Leu	Pro	Arg	Ser	Asn	Ser	Pro	Leu	Ser	
				325					330					335		
Met	Tyr	Arg	Val	Glu	Pro	Ala	Pro	Ile	Pro	Ser	Arg	Lys	Arg	Ala	Phe	
			340					345					350			
Ser	Val	Cys	Ala	Asp	Met	Val	Gly	Ala	Gln	Arg	Glu	Ala	Gly	Met	Val	
		355					360					365				
His	Ala	Asn	Ser	Asp	Thr	Asp	Leu	Thr	Lys	Leu	Asp	Arg	Glu	Lys	Thr	
	370					375					380					
Phe	Glu	Thr	Ala	Glu	Ala	Tyr	His	Gln	Thr	Thr	Asp	Leu	Leu	Ala	Lys	
385					390					395					400	
Val	Val	Asn	Ala	Leu	Ala	Thr	Val	Lys	Pro	Pro	Pro	Ala	Leu	Gln	Glu	
				405					410					415		
Asp	Ala	Ala	Leu	Tyr	Gly	Gly	Tyr	His	Gly	Phe	Ser	Asp	Ser	Gln	Ile	
			420					425					430			
Leu	Ala	Ser	Glu	Trp	Ser	Phe	Ser	Thr	Val	Asn	Glu	Phe	Thr	Ser	Pro	
		435					440					445				
Arg	Arg	Pro	Arg	Ala	Arg	Ala	Cys	Ser	Asp	Phe	Asn	Leu	Glu	Ala	Pro	
	450					455					460					
Arg	Trp	Gln	Ser	Glu	Arg	Pro	Leu	Arg	Ser	Ser	His	Asn	Glu	Trp		
465					470					475						

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Met	Ser	Asp	Gln	Leu	Phe	Val	Ala	Phe	Glu	Lys	Tyr	Phe	Leu	Thr	Ser	
1				5					10					15		
Asn	Glu	Val	Lys	Lys	Asn	Ala	Ala	Thr	Glu	Thr	Trp	Thr	Phe	Ser	Ser	
		20						25					30			

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

TNGGATATCT GGATGACTAT T

21

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

AGTCATCCAG ATAACTCCAG TACTAGTGT

29

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CGCAGGCAGA GCCACAAAGA GTACACAG

28

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GGAGATCAGC TAGGCACCAT ATTTGG

26

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

ATGCTGCATG CCTCATGCTT CCCAGC

26

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GGTTATTTAA AGAGAGGGCT

20

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 426 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Met	Leu	Pro	Ser	Ala	Ser	Arg	Glu	Arg	Pro	Gly	Tyr	Arg	Ala	Gly	Val	
1				5					10					15		
Ala	Ala	Pro	Asp	Leu	Leu	Asp	Pro	Lys	Ser	Ala	Ala	Gln	Asn	Ser	Lys	
			20					25					30			
Pro	Arg	Leu	Ser	Phe	Ser	Thr	Lys	Pro	Thr	Val	Leu	Ala	Ser	Arg	Val	
		35					40					45				
Glu	Ser	Asp	Thr	Thr	Ile	Asn	Val	Met	Lys	Trp	Lys	Thr	Val	Ser	Thr	
	50					55					60					
Ile	Phe	Leu	Val	Val	Val	Leu	Tyr	Leu	Ile	Ile	Gly	Ala	Thr	Val	Phe	
65					70					75					80	
Lys	Ala	Leu	Glu	Gln	Pro	His	Glu	Ile	Ser	Gln	Arg	Thr	Thr	Ile	Val	
				85					90					95		
Ile	Gln	Lys	Gln	Thr	Phe	Ile	Ser	Gln	His	Ser	Cys	Val	Asn	Ser	Thr	
		100						105					110			
Glu	Leu	Asp	Glu	Leu	Ile	Gln	Gln	Ile	Val	Ala	Ala	Ile	Asn	Ala	Gly	
		115					120					125				
Ile	Ile	Pro	Leu	Gly	Asn	Thr	Ser	Asn	Gln	Ile	Ser	His	Trp	Asp	Leu	
	130					135					140					
Gly	Ser	Ser	Phe	Phe	Phe	Ala	Gly	Thr	Val	Ile	Thr	Thr	Ile	Gly	Phe	
145					150					155					160	
Gly	Asn	Ile	Ser	Pro	Arg	Thr	Glu	Gly	Gly	Lys	Ile	Phe	Cys	Ile	Ile	

CGTGCAGCTC	GGAGCGCGCA	GCCCGTCTCT	GAATAAGAAG	TGAGTACAAT	GGCGTGTTTG	120
TAAAAAAAAG	CTTCAAGTCC	GTCTTTTTTCA	AAAAACATTT	TGAATGCTGC	ATGCCTCATG	180
CTTCCCAGCG	CCTCGCGGGA	GAGACCCGGC	TATAGAGCAG	GAGTGGCGGC	ACCTGACTTG	240
CTGGATCCTA	AATCTGCCGC	TCAGAACTCC	AAACCGAGGC	TCTCATTTTC	CACGAAACCC	300
ACAGTGCTTG	CTTCCCAGGT	GGAGAGTGAC	ACGACCATTA	ATGTTATGAA	ATGGAAGACG	360
GTCTCCACGA	TATTCTGGT	GGTTGTCCTC	TATCTGATCA	TCGGAGCCAC	CGTGTTCAAA	420
GCATTGGAGC	AGCCTCATGA	GATTTACACAG	AGGACCACCA	TTGTGATCCA	GAAGCAAACA	480
TTCATATCCC	AACATTCTG	TGTCAATTCTG	ACGGAGCTGG	ATGAACTCAT	TCAGCAAATA	540
GTGGCAGCAA	TAAATGCAGG	GATTATACCG	TTAGGAAACA	CCTCCAATCA	AATCAGTCAC	600
TGGGATTTGG	GAAGTTCCTT	CTTCTTTGCT	GGCACTGTTA	TTACAACCAT	AGGATTTGGA	660
AACATCTCAC	CACGCACAGA	AGGCGGCAAA	ATATTCTGTA	TCATCTATGC	CTTACTGGGA	720
ATTCCCCTCT	TTGGTTTTCT	CTTGGCTGGA	GTTGGAGATC	AGCTAGGCAC	CATATTTGGA	780
AAAGGAATTG	CCAAAGTGGA	AGATACGTTT	ATTAAGTGGA	ATGTTAGTCA	GACCAAGATT	840
CGCATCATCT	CAACAATCAT	ATTTATACTA	TTTGGCTGTG	TACTCTTTGT	GGCTCTGCCT	900
GCGATCATAT	TCAAACACAT	AGAAGGCTGG	AGTGCCCTGG	ACGCCATTTA	TTTTGTGGTT	960
ATCACTCTAA	CAACTATTGG	ATTTGGTGAC	TACGTTGCAG	GTGGATCCGA	TATTGAATAT	1020
CTGGACTTCT	ATAAGCCTGT	CGTGTGGTTC	TGGATCCTTG	TAGGGCTTGC	TTACTTTGCT	1080
GCTGTCCTGA	GCATGATTGG	GAGATTGGTC	CGAGTGATAT	CTAAAAAGAC	AAAAGAAGAG	1140
GTGGGAGAGT	TCAGAGCACA	CGCTGCTGAG	TGGACAGCCA	ACGTCACAGC	CGAATTCAAA	1200
GAAACCAGGA	GGCGACTGAG	TGTGGAGATT	TATGACAAGT	TCCAGCGGGC	CACCTCCATC	1260
AAGCGGAAGC	TCTCGGCAGA	ACTGGCTGGA	AACCACAATC	AGGAGCTGAC	TCCTTGTAGG	1320
AGGACCCTGT	CAGTGAACCA	CCTGACCAGC	GAGAGGGATG	TCTTGCCTCC	CTTACTGAAG	1380
ACTGAGAGTA	TCTATCTGAA	TGGTTTGGCG	CCACACTGTG	CTGGTGAAGA	GATTGCTGTG	1440
ATTGAGAACA	TCAAATAGCC	CTCTCTTTAA	ATAACCTTAG	GCATAGCCAT	AGGTGAGGAC	1500
TTCTCTATGC	TCTTTATGAC	TGTTGCTGGT	AGCATTTTTT	AAATTGTGCA	TGAGCTCAAA	1560
GGGGGAACAA	AATAGATACA	CCCATCATGG	TCATCTATCA	TCAAGAGAAT	TTGGAATTCT	1620
GAGCCAGCAC	TTTCTTTCTG	ATGATGCTTG	TTGAACGGCC	CACTTTCTTT	GATGAGTGGA	1680
ATGACAAGCA	ATGTCTGATG	CCTTTGTGTG	CCCAGACTGT	TTTCCTCTCT	CTTTCCCTAA	1740
TGTGCCATAA	GGCCTCAGAA	TGAATTGAGA	ATTGTTTCTG	GTAACAATGT	AGCTTTGAGG	1800
GATCAGTTCT	TAACTTTTCA	GGGTCTACCT	AACTGAGCCT	AGATATGGAC	CATTTATGGA	1860
TGACAACAAT	TTTTTTTTTG	TAAATGACAA	GAAATTCTTA	TGCAGCCTTT	TACCTAAGAA	1920
ATTTCTGTCA	GTGCCTTATC	TTATGAAGAA	ACAGAACCTC	TCTAGCTAAT	GTGTGGTTTC	1980
TCCTTCCCTG	CCCCACCCC	TAGGCTCACC	TCTGCAGTCT	TTTACCCAG	TTCTCCCATT	2040

TGAATACCAT ACCTTGNTGG AAACAGNGTG TAAAATGACT GAAGTGATGA TGCCGAAGAT 2100
GAAATAGATG NCAAAATTAGN TGGACATTGA 2130

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

AAAAGATCTA AAATGCTTCC CAGCGCC 27

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

AAAGTCGACC TATTTGATGT TCTCAAT 27

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

AAAAAGCTTA AAATGCTTCC CAGCGCC 27

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

AAATCTAGAC TATTTGATGT TCTCAAT

27

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 533 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

AACAAAAACC TTTTTTGT	TTT TGAATGGCCT AGAGAGGGTA AGGGATCCCC TGACGAACAG	60
GAGCAGAGCC AGCTAGAACC TGGGCCTGGC CAGTTCAAGG CCACCAGAGG GCAGCCTTCT		120
GCGGAAGGCA GTATTGGGGT AGGCAGGGAC CCCAGCAGAC ATGGCACTCA GAGCTCTCAC		180
TGTCCACTGA CTCTCTCTTC TCCAGGTTAT GGCCACATGG CCCCACTATC GCCAGGCGGA		240
AAGGCCTTCT GCATGGTCTT ATAGCCCTTG GGCTGCCAGC CTCCTTAGCT CTCGTGGCCA		300
CCCTGCGCCA TTGCCTGCTG CCTGTGCTCA GCCGCCACG TGCCTGGGTA GCGGTCCACT		360
GGCAGCTGTC ACCGGCCAGG GCTGCGCTGC TGCAGGCAGT TGCACTGGGA CTGCTGGTGG		420
CCAGCAGCTT TGTGCTGCTG CCAGCGCTGG TGCTGTGGGG CCTTCAGGGC GACTGCAGCC		480
TGCTGGGGGC CGTCTACTTC TGCTTCAGCT CGCTCAGCAC CATTGGCCTG GGG		533

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 956 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

ATGATACGAT TTAATACGAC TCACTATAGG GAATTTGGCC CTCGAGGCCA AGAATTCGGC	60
ACGAGGAGAA TGTGCGCACG TTGGCTCTCA TCGTGTGCAC CTTACCTAC CTGCTGGTGG	120
GCGCCGCGGT GTTCGACGCA CTGGAGTCGG AGCCGGAGAT GATCGAGCGG CAGCGGCTGG	180
AGCTGCGGCA GCTGGAGCTG CGGGCGCGCT ACAACCTCAG CGAGGGCGGC TACGAGGAGC	240
TGGAGCGCGT CGTGCTGCGC CTCAAGCCGC ACAAGGCCGG CGTGCACTGG CGCTTCGCCC	300
GCTCCTTCTA CTTGCGCATC ACCGTCATCA CCACCATCGG CTATGGTCAT GCGGCGCCCA	360
GCACGGACGG AGGCAAGGTG TTCTGCATGT TCTACGCGCT GCTGGGCATC CCGCTCACAC	420
TAGTCATGTT CCAGAGCCTG GGTGAACGCA TCAACACCTC CGTGAGGTAC CTGCTGCACC	480
GTGCCAAGAG GGGGCTGGGC ATGCGGCACG CCGAAGTGTC CATGGCCAAC ATGGTGCTCA	540

TCGGTTTCGT	GTCGTGCATC	AGCACGCTGT	GCATCGGCGC	AGCTGCCTTC	TCCTACTACG	600
AGCGCTGGAC	TTTCTTCCAG	GCCTATTACT	ACTGCTTCAT	CACCCTCACC	ACCATCGGCT	660
TCGGCGACTA	TGTGGCGCTG	CAGAAGGACC	AGGCGCTGCA	GACGCAGCCG	CAGTATGTGG	720
CTTCAGCTTC	GTGTACATCC	TCACGGGCTC	ACGGTCATCG	GCGCTTCCTC	AACCTCGTGG	780
TGCTGCGATT	CATGACCATG	AACGCCGAGG	ACGAGAAGCG	TGATGCGGAG	CACCGCGCCC	840
TGCTCACGCA	CAACGGCCAG	GCTGTGCGCC	TGGGTGGCCT	GAGCTGCCTG	AGCGGTAGCC	900
TGGGCGACGG	CGTGCGTCCC	CGCGACCCAG	TCACATGCGC	TGCGGCCGCA	AGCTTA	956

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1052 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

CTGAAACCAT	GGGCCCCGATA	CCTGCTCCTG	CTTATGGCCC	ACCTGCTGGC	CATGGGCCTT	60
GGGGCTGTGG	TGCTTCAGGC	CCTGGAGGGC	CCTCCAGCTC	GCCACCTCCA	GGCCCAGGTC	120
CAGGCTGAAC	TGGCTAGCTT	CCAGGCAGAG	CACAGGGCCT	GCTTGCCACC	TGAGGCCCTG	180
GAGGAGCTGC	TAGGTGCGGT	CCTGAGAGCA	CAGGCCCATG	GAGTTTCCAG	CCTGGGCAAC	240
AGCTCAAGAC	AAGCAACTGG	GATCTGCCCT	CAGCTCTGCT	GTTCACTGCC	AGCATCCTCA	300
CCACCACCGG	TTATGGCCAC	ATGGCCCCAC	TCTCCTCAGG	TGGAAAGGCC	TTCTGTGTGG	360
TCTATGCAGC	CCTTGGGCTG	CCAGCCTCTC	TAGCACTTGT	GGCTGCCCTG	CGCCACTGCT	420
TGCTGCCTGT	GTTCAGTCGC	CCAGGTGACT	GGGTAGCCAT	TCGCTGGCAG	CTGGCACCAG	480
CTCAGGCTGC	TCTGCTACAG	GCAGCAGGAC	TGGGCCTCCT	GGTGGCCTGT	GTCTTCATGC	540
TGCTGCCAGC	ACTGGTGCTG	TGGGGTGTA	AGGGTGACTG	GCAGCCTGCT	AAACCATCTA	600
CTTCTGTTTC	GGCTCACTCA	GCACGATCGG	CCTAGGAGAC	TTGCTGCCTG	CCCATGGACG	660
TGGCCTGCAC	CCAGCCATTT	ACCACCTTGG	GCAGTTTGCA	CTTCTTGGTT	ACTTGCTCCT	720
GGGGCTCCTG	GCCATGTTGT	TAGCAGTAGA	GACCTTCTCA	GAGCTGCCTC	AGGTCCGTGC	780
CATGGTGAAA	TTCTTTGGGC	CCAGTGGCTC	TAGAACCGAT	GAAGATCAAG	ATGGCATCCT	840
AGGCCAAGAT	GAGCTGGCTC	TGAGCACTGT	GCTGCCTGAC	GCCCCAGTCT	TGGGACCAAC	900
CACCCCAGCC	TGAGCGGGAG	GCACCAAGGA	GTGCTTGAAG	AACATAGCAG	AAGGGTTATG	960
GGAATGAATA	TGTCATGGGA	TAATGTAAAT	TTTAAAAATT	AAATGGGCTG	CTTAGCATGC	1020
AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AA			1052

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Asn	Lys	Asn	Leu	Phe	Cys	Phe	Glu	Trp	Pro	Arg	Glu	Gly	Lys	Gly	Ser	
1				5					10					15		
Pro	Asp	Gln	Glu	Glu	Gln	Ser	Gln	Leu	Glu	Pro	Gly	Pro	Gly	Gln	Phe	
			20					25					30			
Lys	Ala	Thr	Arg	Gly	Gln	Pro	Ser	Ala	Glu	Gly	Ser	Ile	Gly	Val	Gly	
		35					40					45				
Arg	Asp	Pro	Ser	Arg	His	Gly	Thr	Gln	Ser	Ser	His	Cys	Pro	Leu	Thr	
	50					55					60					
Leu	Ser	Ser	Pro	Gly	Tyr	Gly	His	Met	Ala	Pro	Leu	Ser	Pro	Gly	Gly	
65					70					75					80	
Lys	Ala	Phe	Cys	Met	Val	Leu	Xaa	Ala	Leu	Gly	Leu	Pro	Ala	Ser	Leu	
				85					90					95		
Ala	Leu	Val	Ala	Thr	Leu	Arg	His	Cys	Leu	Leu	Pro	Val	Leu	Ser	Arg	
			100					105					110			
Pro	Arg	Ala	Trp	Val	Ala	Val	His	Trp	Gln	Leu	Ser	Pro	Ala	Arg	Ala	
		115					120					125				
Ala	Leu	Leu	Gln	Ala	Val	Ala	Leu	Gly	Leu	Leu	Val	Ala	Ser	Ser	Phe	
		130				135					140					
Val	Leu	Leu	Pro	Ala	Leu	Val	Leu	Trp	Gly	Leu	Gln	Gly	Asp	Cys	Ser	
145					150					155					160	
Leu	Leu	Gly	Ala	Val	Tyr	Phe	Cys	Phe	Ser	Ser	Leu	Ser	Thr	Ile	Gly	
				165					170					175		
Leu	Gly															

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Gly	Ile	Trp	Pro	Ser	Arg	Pro	Arg	Ile	Arg	His	Glu	Glu	Asn	Val	Arg	
1				5					10					15		
Thr	Leu	Ala	Leu	Ile	Val	Cys	Thr	Phe	Thr	Tyr	Leu	Leu	Val	Gly	Ala	

20										25					30															
Ala	Val	Phe	Asp	Ala	Leu	Glu	Ser	Glu	Pro	Glu	Met	Ile	Glu	Arg	Gln															
		35					40					45																		
Arg	Leu	Glu	Leu	Arg	Gln	Leu	Glu	Leu	Arg	Ala	Arg	Tyr	Asn	Leu	Ser															
	50					55					60																			
Glu	Gly	Gly	Tyr	Glu	Glu	Leu	Glu	Arg	Val	Val	Leu	Arg	Leu	Lys	Pro															
65					70					75					80															
His	Lys	Ala	Gly	Val	Gln	Trp	Arg	Phe	Ala	Gly	Ser	Phe	Tyr	Phe	Ala															
				85				90					95																	
Ile	Thr	Val	Ile	Thr	Thr	Ile	Gly	Tyr	Gly	His	Ala	Ala	Pro	Ser	Thr															
			100				105						110																	
Asp	Gly	Gly	Lys	Val	Phe	Cys	Met	Phe	Cys	Met	Phe	Tyr	Ala	Leu	Leu															
		115					120					125																		
Gly	Ile	Pro	Leu	Thr	Leu	Val	Met	Phe	Gln	Ser	Leu	Gly	Glu	Arg	Ile															
	130					135					140																			
Asn	Thr	Ser	Val	Arg	Tyr	Leu	Leu	His	Arg	Ala	Lys	Arg	Gly	Leu	Gly															
145					150				155						160															
Met	Arg	His	Ala	Glu	Val	Ser	Met	Ala	Asn	Met	Val	Leu	Ile	Gly	Phe															
				165					170					175																
Val	Ser	Cys	Ile	Ser	Thr	Leu	Cys	Ile	Gly	Ala	Ala	Ala	Phe	Ser	Tyr															
			180				185						190																	
Tyr	Glu	Arg	Trp	Thr	Phe	Phe	Gln	Ala	Tyr	Tyr	Tyr	Cys	Phe	Ile	Thr															
		195					200					205																		
Leu	Thr	Thr	Ile	Gly	Phe	Gly	Asp	Tyr	Val	Ala	Leu	Gln	Lys	Asp	Gln															
	210					215					220																			
Ala	Leu	Gln	Thr	Gln	Pro	Gln	Tyr	Val	Ala	Ser	Ala	Ser	Cys	Thr	Ser															
225					230					235					240															
Ser	Arg	Ala	His	Gly	His	Arg	Arg	Phe	Leu	Asn	Leu	Val	Val	Leu	Arg															
				245					250					255																
Phe	Met	Thr	Met	Asn	Ala	Glu	Asp	Glu	Lys	Arg	Asp	Ala	Glu	His	Arg															
			260					265					270																	
Ala	Leu	Leu	Thr	His	Asn	Gly	Gln	Ala	Val	Gly	Leu	Gly	Gly	Leu	Ser															
		275					280					285																		
Cys	Leu	Ser	Gly	Ser	Leu	Gly	Asp	Gly	Val	Arg	Pro	Arg	Asp	Pro	Val															
	290					295					300																			
Thr	Cys	Ala	Ala	Ala	Ala	Ser	Leu																							
305						310																								

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Leu	Lys	Pro	Trp	Ala	Arg	Tyr	Leu	Leu	Leu	Leu	Met	Ala	His	Leu	Leu	
1				5					10					15		
Ala	Met	Gly	Leu	Gly	Ala	Val	Val	Leu	Gln	Ala	Leu	Glu	Gly	Pro	Pro	
			20					25					30			
Ala	Arg	His	Leu	Gln	Ala	Gln	Val	Gln	Ala	Glu	Leu	Ala	Ser	Phe	Gln	
		35					40					45				
Ala	Glu	His	Arg	Ala	Cys	Leu	Pro	Pro	Glu	Ala	Leu	Glu	Glu	Leu	Leu	
	50					55					60					
Gly	Ala	Val	Leu	Arg	Ala	Gln	Ala	His	Gly	Val	Ser	Ser	Leu	Gly	Asn	
65					70				75						80	
Ser	Ser	Xaa	Thr	Ser	Asn	Trp	Asp	Leu	Pro	Ser	Ala	Leu	Leu	Phe	Thr	
				85					90					95		
Ala	Ser	Ile	Leu	Thr	Thr	Thr	Gly	Tyr	Gly	His	Met	Ala	Pro	Leu	Ser	
			100					105					110			
Ser	Gly	Gly	Lys	Ala	Phe	Cys	Val	Val	Tyr	Ala	Ala	Leu	Gly	Leu	Pro	
		115					120					125				
Ala	Ser	Leu	Ala	Leu	Val	Ala	Ala	Leu	Arg	His	Cys	Leu	Leu	Pro	Val	
	130					135					140					
Phe	Ser	Arg	Pro	Gly	Asp	Trp	Val	Ala	Ile	Arg	Trp	Gln	Leu	Ala	Pro	
145					150					155					160	
Ala	Gln	Ala	Ala	Leu	Leu	Gln	Ala	Ala	Gly	Leu	Gly	Leu	Leu	Val	Ala	
				165					170					175		
Cys	Val	Phe	Met	Leu	Leu	Pro	Ala	Leu	Val	Leu	Trp	Gly	Val	Gln	Gly	
			180					185					190			
Asp	Trp	Gln	Pro	Ala	Xaa	Thr	Ile	Tyr	Phe	Cys	Phe	Gly	Ser	Leu	Ser	
		195					200					205				
Thr	Ile	Gly	Leu	Gly	Asp	Leu	Leu	Pro	Ala	His	Gly	Arg	Gly	Leu	His	
	210					215					220					
Pro	Ala	Ile	Tyr	His	Leu	Gly	Gln	Phe	Ala	Leu	Leu	Gly	Tyr	Leu	Leu	
225					230					235					240	
Leu	Gly	Leu	Leu	Ala	Met	Leu	Leu	Ala	Val	Glu	Thr	Phe	Ser	Glu	Leu	
				245					250					255		
Pro	Gln	Val	Arg	Ala	Met	Val	Lys	Phe	Phe	Gly	Pro	Ser	Gly	Ser	Arg	
			260					265					270			
Thr	Asp	Glu	Asp	Gln	Asp	Gly	Ile	Leu	Gly	Gln	Asp	Glu	Leu	Ala	Leu	
	275						280					285				
Ser	Thr	Val	Leu	Pro	Asp	Ala	Pro	Val	Leu	Gly	Pro	Thr	Thr	Pro	Ala	
	290					295					300					